

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 14:56:27 ; Search time 14 Seconds
(without alignments)
1679.791 Million cell updates/sec

Title: US-08-813-323b-1

Perfect score: 2294
Sequence: 1 MESSKKMDAAGTLQNPPLK.....IKDDTIFIKYVDTSLPDP 567

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2994	100.0	567	1	TRA3_MOUSE
2	2886.5	96.4	567	1	TRA3_MOUSE
3	837.5	28.0	501	1	TRA2_MOUSE
4	745.5	24.9	501	1	TRA2_MOUSE
5	641.5	21.4	416	1	TRA1_MOUSE
6	640	21.4	409	1	TRA1_MOUSE
7	209	7.0	458	1	DG17_DICD1
8	168	5.6	1816	1	LMA4_MOUSE
9	164	5.5	919	1	RA50_AERPE
10	161	5.4	634	1	MYSC_CHICK
11	157.5	5.3	1102	1	MEPB_MOUSE
12	151.5	5.1	704	1	MEPB_MOUSE
13	149	5.0	1957	1	YDB6_SCHPO
14	147	4.9	1816	1	LMA4_MOUSE
15	147	4.9	2230	1	GOG4_HUMAN
16	147	4.9	3210	1	CENF_HUMAN
17	146	4.9	1679	1	Y109_YEAST
18	146	4.9	1727	1	ALM1_SCHPO
19	145.5	4.9	944	1	NUP1_YEAST
20	145	4.8	624	1	A33_PLEMA
21	145	4.8	1005	1	RA50_METJA
22	144.5	4.8	425	1	TM31_HUMAN
23	144	4.8	1935	1	MYH7_RAT
24	142.5	4.8	794	1	HMNR_MOUSE
25	142.5	4.8	1940	1	MYH3_RAT
26	141.5	4.7	1935	1	MYH7_HUMAN
27	141	4.7	1940	1	MYH3_CHICK
28	140.5	4.7	886	1	RA50_ARCFU
29	140.5	4.7	1934	1	MYH7_MESAU
30	140	4.7	879	1	RA50_PYROH
31	139.5	4.7	1940	1	MYH3_HUMAN
32	139	4.6	1790	1	USO1_YEAST
33	139	4.6	1938	1	MYH3_HUMAN

34	138.5	4.6	886	1	RA50_SULAC
35	137	4.6	1046	1	SBCA_LACLA
36	137	4.6	1935	1	MYSC_CYPRA
37	136.5	4.6	551	1	RN27_MOUSE
38	136.5	4.6	1935	1	MYH7_PIG
39	136.5	4.6	1935	1	MYH6_HUMAN
40	136	4.5	704	1	MEPB_RAT
41	136	4.5	1941	1	MYH2_HUMAN
42	135	4.5	390	1	TFP1_BOVIN
43	133.5	4.5	852	1	RA50_THEMA
44	133.5	4.5	999	1	CARE_MOUSE
45	133.5	4.5	1084	1	MYSS_RABIT

ALIGNMENTS

RESULT 1
TRA3_MOUSE
ID TRA3_MOUSE STANDARD: PRT: 567 AA.

AC 060803: 062380:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
DE (CRAFT) (TRAFAFMN).
CN TRAF3 OR CRAFT OR TRAFAMN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAFT, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).

[2]
RN SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RP STRAIN=C57BL/6J; TISSUE=Brain;
RC MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
RA Dinulos M.B., Distche C.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Lacy E.;
RT "A candidate gene for the amniotless gastrulation stage mouse mutation
RT encodes a TRAF-related protein.";
RL Dev. Biol. 177:374-390(1996).

- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).
- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
ASSOCIATED FACTORS (POTENTIAL).
- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN
KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
FOUND IN LIVER.
- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5, HIGHEST
LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.

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or send an email to license@sib-sib.ch).

EMBL: U21050; AAC52175.1; -
EMBL: U33840; AAC52710.1; -
MGI: 108041; Traf3.

DR InterPro: IPR002083; MATH.
 DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; ZnF-TRAF.
 DR InterPro: IPR001841; ZnF-ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR PROSITE: PS50145; ZF-TRAF; 2.
 DR Zinc-finger: Coiled coil; Repeat.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 67 76 RING-TYPE.
 FT ZN_FING 134 189 TRAF-TYPE 1.
 FT ZN_FING 190 248 TRAF-TYPE 2.
 FT DOMAIN 266 337 COILED COIL (POTENTIAL).
 FT DOMAIN 417 502 MATH/TRAF.
 FT CONFLICT 72 73 CE -> WO (IN REF. 2).
 FT CONFLICT 390 390 T -> M (IN REF. 2).
 SQ SEQUENCE 567 AA: 64263 MW: 25228343841192DC CRC64;

Query Match 100.0%; Score 2994; DB 1; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.3e-172;
 Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MESSKMDAGTLPNPPLKLOPRDAGSVLPEDGGYKREKFKVTEDEKYEKCRALYC 60
 DB 1 MESSKMDAGTLPNPPLKLOPRDAGSVLPEDGGYKREKFKVTEDEKYEKCRALYC 60
 OY 61 NKQTECGHRCFECSCMAALLSSSSPKCTACQESITKDKVFNCKCKRELLAQVYCRNEG 120
 DB 61 NKQTECGHRCFECSCMAALLSSSSPKCTACQESITKDKVFNCKCKRELLAQVYCRNEG 120
 OY 121 RCGAEOLTLGHLVHLKNECCFEELPCIRADCKEVLKDLRDHYEKCKTREATCSCK 180
 DB 121 RCGAEOLTLGHLVHLKNECCFEELPCIRADCKEVLKDLRDHYEKCKTREATCSCK 180
 OY 181 SOVPMIKLQKHEDTDCPCVAVSCPHKCSVQTLRLSELSAHLSECVNAPSTCSFKRYGVF 240
 DB 181 SOVPMIKLQKHEDTDCPCVAVSCPHKCSVQTLRLSELSAHLSECVNAPSTCSFKRYGVF 240
 OY 181 SOVPMIKLQKHEDTDCPCVAVSCPHKCSVQTLRLSELSAHLSECVNAPSTCSFKRYGVF 240
 DB 181 SOVPMIKLQKHEDTDCPCVAVSCPHKCSVQTLRLSELSAHLSECVNAPSTCSFKRYGVF 240
 OY 241 OGTOQITAHESASAVQVHNLKESNSLEKRVSLLONESEYKKNSTIOSLHNOJCSFEIE 300
 DB 241 OGTOQITAHESASAVQVHNLKESNSLEKRVSLLONESEYKKNSTIOSLHNOJCSFEIE 300
 OY 301 IEROKEMLRNNESEKILHLQVYIDSOAEKLEDEIRPEFRONWEEADSMKSSVESLQNRV 360
 DB 301 IEROKEMLRNNESEKILHLQVYIDSOAEKLEDEIRPEFRONWEEADSMKSSVESLQNRV 360
 OY 361 TELESVDKSAGQAARNGLLESQLSRHDQTLVSHDIRLADMDLRFQVLETASYNGVLIWK 420
 DB 361 TELESVDKSAGQAARNGLLESQLSRHDQTLVSHDIRLADMDLRFQVLETASYNGVLIWK 420
 OY 421 IRDVKRRQEAQVNGKTLSTYSQPYTGYGKMKCARVYLYLNDGNGKSTHLSLFFVIMRGE 480
 DB 421 IRDVKRRQEAQVNGKTLSTYSQPYTGYGKMKCARVYLYLNDGNGKSTHLSLFFVIMRGE 480
 OY 481 YDALPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSRKPKPGEMNINASGCVFYAQT 540
 DB 481 YDALPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSRKPKPGEMNINASGCVFYAQT 540
 OY 541 VLENGTYIKDDTIFIKYIVDTSLDLPD 567
 DB 541 VLENGTYIKDDTIFIKYIVDTSLDLPD 567

RESULT 2
 TRAF3_HUMAN STANDARD; PRT; 568 AA.
 AC Q13114; Q13076; Q13947; Q12990;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-TUN-2002 (Rel. 41, Last annotation update)
 DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
 DE (CRAFT) (CD40 binding protein) (CD40BP) (LMP1 associated protein)
 DE (LMP1) (CAP-1).
 GN TRAF3 OR CRAFT OR CAP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95184010; PubMed-7533327;
 RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
 RT "Involvement of CRAFT, a relative of TRAF, in CD40 signalling.";
 RL Science 267:1494-1498(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE-95163092; PubMed-7859281;
 RA Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
 RA Kieff E.;
 RT "The Epstein-Barr virus transforming protein LMP1 engages signaling
 RT proteins for the tumor necrosis factor receptor family.";
 RL Cell 80:389-399(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Fetal brain;
 RX MEDLINE-95129692; PubMed-7530216;
 RA Sato T., Irie S., Reed J.C.;
 RT "A novel member of the TRAF family of putative signal transducing
 RT proteins binds to the cytosolic domain of CD40.";
 RL FIBS Lett. 358:113-118(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95073988; PubMed-7527023;
 RA Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;
 RT "A novel RING finger protein interacts with the cytoplasmic domain of
 RT CD40.";
 RL J. Biol. Chem. 269:30069-30072(1994).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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 CC -----
 DR EMBL: U01092; AAC50112.1; -
 DR EMBL: U19260; AAA65732.1; -
 DR EMBL: U38509; AAA68195.1; -
 DR EMBL: U15637; AAA56753.1; -
 DR Genew; HGNC:12033; TRAF3.
 DR MIM: 601896; -
 DR InterPro: IPR002083; MATH.
 DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; ZnF-TRAF.
 DR InterPro: IPR001841; ZnF-ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.

DR PROSITE: PS50145; ZF-TRAF; 2.
 KW Zinc-finger: Coiled coil; Repeat.
 FT ZN_FING 68 77 RING-TYPE.
 FT ZN_FING 135 190 TRAF-TYPE 1.
 FT ZN_FING 191 249 TRAF-TYPE 2.
 FT DOMAIN 267 338 COILED COIL (POTENTIAL).
 FT DOMAIN 418 503 COILED COIL (POTENTIAL).
 FT DOMAIN 129 129 T -> M (IN REF. 2 AND 4).
 FT CONFLICT 134 134 MISSING (IN REF. 4).
 FT CONFLICT 218 242 MISSING (IN REF. 3).
 FT CONFLICT 339 339 P -> S (IN REF. 3).
 FT CONFLICT 405 405 R -> G (IN REF. 4).
 SO SEQUENCE 568 AA: 64460 MW: 6765533BPF23C8B CRC64;

Query Match 96.4%; Score 2886.5; DB 1; Length 568;
 Best Local Similarity 96.1%; Pred. No. 3,7e-166;
 Matches 546; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

OY 1 MESSKMDAAGTLPNPPLKLPDPRGAGS-VLVEGCGYKKEFKYEDKYEKCKRLYL 59
 DB 1 MESSKMDSPGALQTNPLKLTDRSAGTPVFEQGGYKKEFKYEDKYEKCKRLYL 60
 OY 60 CRRPTEGHRCECSCMAALLSSSPKCTACQESITIKDKYFKDCKREILALQVYCRNE 119
 DB 61 CRRPTEGHRCECSCMAALLSSSPKCTACQESITIKDKYFKDCKREILALQVYCRNE 120
 OY 120 GRCACQTLGLHLVHLNCEQFELPCLRADCKEYLRKDLRDHVERKACKYREATCSHC 179
 DB 121 SRGCAQDLTGLHLVHLNCEQFELPCVRPDCKEKYLKDLRDHVERKACKYREATCSHC 180
 OY 180 KQGVPMIKLQKHEDTDCPCVAVSCPHKCSVQTLRLSELTAHLSCVNAFSTCSKRYGCV 239
 DB 181 KQGVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELTAHLSCVNAFSTCSKRYGCV 240
 OY 240 FQGTNOQIAHFASSAVQVNLKREMSNLEKYSVLQNESVEKNKSIOSLHNOICSEI 299
 DB 241 FQGTNOQIAHFASSAVQVNLKREMSNLEKYSVLQNESVEKNKSIOSLHNOICSEI 300
 OY 300 EIEROKEMLRNNEKTLQLQVYDSQAEKLEKEIRPFQNMNEADSMKSVESIQNR 359
 DB 301 EIEROKEMLRNNEKTLQLQVYDSQAEKLEKEIRPFQNMNEADSMKSVESIQNR 360
 OY 360 VTELESVDKASAGAVNRGTLSESLRHDQTSVHDIRLADMDLRFQVLETASYNGVLIW 419
 DB 361 VTELESVDKASAGAVNRGTLSESLRHDQTSVHDIRLADMDLRFQVLETASYNGVLIW 420
 OY 420 KIRDYRRKQEAVMKTLISLVSQPEYTGEGYKMCARVYLNGDGKGTSLFFVIMRG 479
 DB 421 KIRDYRRKQEAVMKTLISLVSQPEYTGEGYKMCARVYLNGDGKGTSLFFVIMRG 480
 OY 480 EYDALLPMPKQKVITLMDQSSRRHLDARPDNNSSEFKKPTGENNIASGCVFVAQ 539
 DB 481 EYDALLPMPKQKVITLMDQSSRRHLDARPDNNSSEFKKPTGENNIASGCVFVAQ 540
 OY 540 TVLENGTYIKDPTIFIKVIVDTSDDLP 567
 DB 541 TVLENGTYIKDPTIFIKVIVDTSDDLP 568

RESULT 3
 TRAF2 MOUSE
 ID TRAF2 MOUSE STANDARD: PRT; 501 AA.
 AC P39439;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TNF receptor associated factor 2 (TRAF2).
 GN TRAF2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94349371; PubMed=8069916;
 RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RL cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 CC Cell 78:681-692(1994).
 CC -FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
 CC ACTIVATES NF-KAPPA-B.
 CC -SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
 CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
 CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
 CC FACTOR RECEPTOR 2 (TNFR2).
 CC -SUBCELLULAR LOCATION: Cytoplasmic.
 CC -SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
 CC -SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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DR EMBL: L35303; AAC37662.1; -
 DR HSSP: P12351; 1HWT.
 DR MGD: MGI:101835; Traf2.
 DR InterPro: IPR002083; MATH.
 DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; Znf-TRAF.
 DR InterPro: IPR001841; Znf-fing.
 DR Pfam: PF00097; ZF-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; ZF-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF-RING-1; 1.
 DR PROSITE: PS50089; ZF-RING-2; 1.
 DR PROSITE: PS50145; ZF-TRAF; 2.
 KW Zinc-finger: Coiled coil; Repeat.
 FT ZN_FING 34 73 RING-TYPE.
 FT ZN_FING 124 180 TRAF-TYPE 1.
 FT ZN_FING 177 233 TRAF-TYPE 2.
 FT DOMAIN 298 348 COILED COIL (POTENTIAL).
 FT DOMAIN 334 501 MATH/TRAF.
 SO SEQUENCE 501 AA: 56026 MW: 043B391180365F10 CRC64;

Query Match 28.0%; Score 837.5; DB 1; Length 501;
 Best Local Similarity 33.5%; Pred. No. 2.3e-43;
 Matches 194; Conservative 88; Mismatches 196; Indels 99; Gaps 16;

OY 7 MDAAGTLPNPPLKLPDPRGAGSVLVEGCGYKKEFKYEDKYEKCKRLYLCPKQT 65
 DB 1 MAAATYSRGSLELDP-----GFSKTLTGRLKAKYLGCKNKLRLRPPQA 47
 OY 66 ECGHRCECSCMAALLSSSPKCTAC-----QESIT--KDKYFKDCKREILALQVYCR 116
 DB 48 QCGHRCECSCMAALLSSSPKCTAC-----QESIT--KDKYFKDCKREILALQVYCR 107
 OY 117 RNEGRCAQDLTGLHLVHLNCEQFELPCLRADCKEYLRKDLRDHVERKACKYREATC 176
 DB 108 PND--GCTWRGTLKEYESCHEGLCPRLTEC--PAKGLVLRSEKHTEDQCPKRSLSG 163
 OY 177 SHCKSQVPMIKLQKHEDTDCPCVAVSCPHKCSVQTLRLSELTAHLSECYNASTCSFRY 236
 DB 164 QHCAPCSHVDLEHYEV--CPKPLTC--DQCGKKKIPREFPDHVRACSKCVLCRFHTV 221
 OY 237 GCYFGTNOQIAHFASSAVQVNLKREMSNLEKYSVLQNESVEKNKSIOSLHNOICSEI 286
 DB 222 GCSEVETENLQDHEIOLREHALL--LSSFLQASGPTLNQVGPPELLQRCQILLEOR- 278

QY 287 IQSLHNOICFEIEIEROKEMLNNESEKILHLQVRIDVSOAEKIKELDKETRPRQNWEEA 346
 Db 279 IAFENIVCLNREVER-----VAYAEACSQHRLDD----- 312
 QY 347 DSKSSVESIQNRVTELESVDKSGAARNLTGLLESQLSRHDTLSVHDIRLADMLRFQ 406
 Db 313 -----KIEALSNKVQOLE-----RSIGLMDLMAADLEQKVS 343
 QY 407 VLETAASYNGVLIWKIRIDYKRROEAVMGKTLISYQOPFYTGFGKMKARVYLNDGCK 466
 Db 344 ELEFSTYDGVETIKISDFRRKROEAVAGTPAIFSPATYSRYGKMLRYLNDGDTGR 403
 QY 467 GTHLSLFVYIMRGEVDALLPMPFKOKVITLMDQSSRRHLGDAKPDPNSSFPKPTGE 526
 Db 404 GTHLSLFVYIMRGEVDALLPMPFKOKVITLMDLH-NRNEHVIDARPDVTSSTFORPVS 462
 QY 527 MNIASGCPVFAQVLE-NGTYIKDITFIKVIYDTSPL 564
 Db 463 MNIASGCPVFAQVLE-NGTYIKDITFIKVIYDTSPL 501

RESULT 4

TRAF2_HUMAN STANDARD: PRT; 501 AA.
 AC Q12933;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TNF receptor associated factor 2 (TRAF2) (Tumor necrosis factor type 2 receptor associated protein 3).
 GN TRAF2 OR TRAF3.

OS Homo sapiens (Human).
 OC Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RP MEDLINE=95366958; PubMed=7639698;
 RA Song H.Y., Donner D.B.;

RT "Association of a RING finger protein with the cytoplasmic domain of the human type-2 tumour necrosis factor receptor.";
 RL Biochem. J. 309:825-829(1995).
 RN [2]

RP MEDLINE=94349371; PubMed=8069916;
 RA Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;

RT "A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RN [1]

CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND ACTIVATES NF-KAPPA-B.

CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEIN 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.

CC -----
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CC -----
 DR EMBL: U12597; AAA87706.1;
 DR GenBank: HGNC:12032; TRAF2.
 DR MIM: 601895;
 DR InterPro: IPR002083; MATH.

DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; Znf-TRAF.
 DR InterPro: IPR001841; Znf-TRAF.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF-RING-1; 2.
 DR PROSITE: PS00089; ZF-RING-2; 1.
 DR PROSITE: PS0145; ZF-TRAF; 2.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 34 73 RING-TYPE.
 FT ZN_FING 124 180 TRAF-TYPE 1.
 FT ZN_FING 177 233 TRAF-TYPE 2.
 FT DOMAIN 299 348 COILED COIL (POTENTIAL).
 FT DOMAIN 334 501 MATH/TRAF.
 FT CONFLICT 343 365 RFDQAGHRICSFCLASILRLK -> LEMEASTYDGVPIW
 FT KISDFARRK (IN REF. 2).
 SQ SEQUENCE 501 AA; 55794 MW; 8883651EB6E20743 CRC64;

Query Match 24.9%; Score 745.5; DB 1; Length 501;
 Best Local Similarity 32.1%; Pred. No. 7.5e-38;
 Matches 188; Conservative 92; Mismatches 194; Indels 111; Gaps 21;

QY 7 MDAAGTLQNPPLKIQPRGAGSVLPBGGYKKEFKVT-VEDEKYCEKRLVLCNPKRT 65
 Db 1 MAASVTPPGSLLELLP-----GFSKTLGTLEAKVLYCSACRNVLRPFQA 47
 QY 66 ECGHRCESCMALISLSSSPKCTAC-GEITIKDV-----FKMCCRELLAQVYC 116
 Db 48 QCGHRCESCMALISLSSSPKCTAC-GEITIKDV-----FKMCCRELLAQVYC 107
 QY 117 RNEGFGCAEQTLTGLHLVHLKNEQFELPCLRAD--CKEYLRKDLRDHYEACKYRE 173
 Db 108 PSD-GCTWKGTLKEY-----ESCHGRCPMLTEPCAGGLVRLBEKHEHLEHECPERS 160
 QY 174 ATCSHCKSQVPMITLOKHEDTDCVAVVSCPHKCSQVTLRLSLASHLSECVNAPSTGCF 233
 Db 161 LSCRHCRAPCCGADVKAHHEV-CPKPLTC-DGCGKKRIPREFODHYTCGCRVPCRF 218
 QY 234 KRYGVV--FGTNOQIRAHSSAVQVNLKEMSNLEKK-----VSLQD-ES 280
 Db 219 HAIGCLETFVEGEKQ--EHEVQWLRHLAML--LSVLEKAPLIGQSHAGSEILLQRCSS 274
 QY 281 VEKKKSQSLHNOICFEIEIEROKEMLNNESEKILHLQVRIDVSOAEKIKELDKETRPR 340
 Db 275 LEKRTA--TRENIVCLNREVER-----VAMTAACS-----R 305
 QY 341 QNWEADSMKSSVESIQNRVTELESVDKSGAARNLTGLLESQLSRHDTLSVHDIRLAD 400
 Db 306 QHRLDD-----KIEALSNKVQOLE-----RSIGLMDLMAAD 337
 QY 401 MDLRFQVLETAASYNGVLIWKIRIDYKRROEAVMGKTLISYQOPFYTGFGKMKARVYL 460
 Db 338 LEQVRFPOAQCHRYCSFCLASILRLKLOEAVAGRIPAIFSPATYSRYGKMLRYLNDG 397
 QY 461 GDGKGKSTHLSLFVYIMRGEVDALLPMPFKOKVITLMDQSSRRHLGDAKPDPNSSSF 520
 Db 398 GDGGRKSTHLSLFVYIMRGEVDALLPMPFKOKVITLMDLH-NRNEHVIDARPDVTSST 456
 QY 521 KPTGEMNIASGCPVFAQVLE-NGTYIKDITFIKVIYDTSPL 564
 Db 457 QRPVNDMNIASGCPVFAQVLE-NGTYIKDITFIKVIYDTSPL 501

RESULT 5

TRAF2_HUMAN STANDARD: PRT; 416 AA.
 AC Q13077;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

Query Match	7.0%;	Score 209;	DB 1;	Length 458;
Best Local Similarity	20.3%;	Pred. No. 1e-05;		
Matches 115;	Conservative	80;	Mismatches 177;	Indels 194;
				Gaps 27;

RESULT 8	LMA4_MOUSE	STANDARD:	PRT;	1816 AA.
ID	LMA4_MOUSE	P97927; P70409; 088785;		
AC	P97927; P70409; 088785;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	laminin alpha-4 chain precursor.			
CN	LAMA4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
LN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND 940-945.			
RC	STRAIN=BALB/c; TISSUE=Endothelial cells;			
RC	MEDLINE=97363207; PubMed=9219532;			
RA	Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R., Sorokin L.M.;			
RA	"Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of endothelium.";			
RT	Eur. J. Biochem. 246:727-735(1997).			
LN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RC	MEDLINE=97202462; PubMed=9049981;			
RA	Liu J., Mayne R.;			
RA	"The complete cDNA coding sequence and tissue-specific expression of the mouse laminin alpha 4 chain.";			
RT	Matrix Biol. 15:433-437(1996).			
LN				

[3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=98010627; PubMed=9346933;
 RA Iivanainen A., Kortasmaa J., Sahlgren C., Morita T., Bergmann U.,
 RA Thelieff I., Tryggvason K.;
 RT "Primary structure, developmental expression, and immunolocalization
 of the murine laminin alpha4 chain.";
 RL J. Biol. Chem. 272:27862-27868(1997).
 RN [4]
 RP SEQUENCE OF 836-1106 FROM N.A.
 RC STRAIN-ICR; TISSUE=Placenta;
 RX MEDLINE=97296337; PubMed=9151674;
 RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Saes J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 chromosomal locations of alpha-5, identification of heterotrimeric
 laminins 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-702(1997).
 RN [5]
 RP SEQUENCE OF 1467-1691 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97187457; PubMed=9034910;
 RA Lentz S.I., Miner J.H., Saes J.R., Snider W.D.;
 RT "Distribution of the ten known laminin chains in the pathways and
 targets of developing sensory axons.";
 RL J. Comp. Neurol. 378:547-561(1997).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration, and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
 MEMBRANES (MAJOR COMPONENT).
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PERIPHERAL NERVES,
 CARDIAC MUSCLE, FAT, DERMIS, LUNG STROMA, AORTIC ENDOTHELIUM,
 ENDOCARDIUM AND ENDOTHELIDUM OF BLOOD VESSELS IN SKIN AND BRAIN.
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
 CC -1- SIMILARITY: CONTAINS 3.5 LAMININ EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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 CC -----
 DR EMBL: U58950; AABA1840.1; -
 DR EMBL: Y09827; CAAT0970.1; -
 DR EMBL: U59865; AAC24725.1; -
 DR EMBL: U88352; AAC53178.1; -
 DR EMBL: U69176; AAC52982.1; -
 DR HSSP: P02468; IKLO.
 DR MGD: MGI:109321; Lama4.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00053; Laminin_EGF; 3.
 DR Pfam: PF00054; Laminin_G; 4.
 DR SMART: SM00181; EGF; 3.
 DR PROSITE: PS00022; EGF_1; UNKNOWN.1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 3.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 5.
 DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	1816	LAMININ ALPHA-4 CHAIN.
FT	DOMAIN	82	131	LAMININ EGF-LIKE 1.
FT	DOMAIN	132	186	LAMININ EGF-LIKE 2.
FT	DOMAIN	187	240	LAMININ EGF-LIKE 3.
FT	DOMAIN	241	255	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT	DOMAIN	256	825	LAMININ II AND I.
FT	DOMAIN	826	1030	LAMININ G-LIKE 1.
FT	DOMAIN	1042	1222	LAMININ G-LIKE 2.
FT	DOMAIN	1229	1397	LAMININ G-LIKE 3.
FT	DOMAIN	1462	1633	LAMININ G-LIKE 4.
FT	DOMAIN	1640	1813	LAMININ G-LIKE 5.
FT	DOMAIN	431	523	COILED COIL (POTENTIAL).
FT	DOMAIN	556	604	COILED COIL (POTENTIAL).
FT	DOMAIN	655	717	COILED COIL (POTENTIAL).
FT	DOMAIN	770	799	COILED COIL (POTENTIAL).
FT	STATE	717	719	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	82	91	BY SIMILARITY.
FT	DISULFID	84	98	BY SIMILARITY.
FT	DISULFID	101	110	BY SIMILARITY.
FT	DISULFID	113	129	BY SIMILARITY.
FT	DISULFID	132	146	BY SIMILARITY.
FT	DISULFID	134	155	BY SIMILARITY.
FT	DISULFID	157	166	BY SIMILARITY.
FT	DISULFID	169	184	BY SIMILARITY.
FT	DISULFID	187	202	BY SIMILARITY.
FT	DISULFID	189	209	BY SIMILARITY.
FT	DISULFID	212	221	BY SIMILARITY.
FT	DISULFID	224	238	BY SIMILARITY.
FT	DISULFID	266	266	INTERCHAIN (PROBABLE).
FT	DISULFID	269	269	INTERCHAIN (PROBABLE).
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	215	215	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	308	308	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	333	333	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	338	338	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	550	550	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	571	571	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	574	574	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	639	639	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	735	735	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	751	751	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	754	754	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	780	780	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	803	803	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1283	1283	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1361	1361	N-LINKED (GLCNAC. . .)
FT	CONFLICT	8	8	C -> S (IN REF. 2).
FT	CONFLICT	18	18	C -> Y (IN REF. 2).
FT	CONFLICT	248	248	G -> R (IN REF. 3).
FT	CONFLICT	297	297	G -> A (IN REF. 3).
FT	CONFLICT	431	433	THR -> HPS (IN REF. 2).
FT	CONFLICT	679	679	S -> C (IN REF. 3).
FT	CONFLICT	703	703	D -> G (IN REF. 2).
FT	CONFLICT	706	706	N -> H (IN REF. 2).
FT	CONFLICT	728	728	K -> R (IN REF. 2).
FT	CONFLICT	730	730	F -> I (IN REF. 2).
FT	CONFLICT	779	779	R -> G (IN REF. 1).
FT	CONFLICT	810	810	R -> S (IN REF. 3).
FT	CONFLICT	865	867	AEP -> QT (IN REF. 2).
FT	CONFLICT	936	936	K -> E (IN REF. 3).
FT	CONFLICT	970	970	L -> V (IN REF. 3).
FT	CONFLICT	1132	1132	H -> R (IN REF. 2).
FT	CONFLICT	1200	1200	F -> I (IN REF. 2).
FT	CONFLICT	1382	1382	D -> A (IN REF. 2).
FT	CONFLICT	1413	1414	NS -> EF (IN REF. 1).
FT	CONFLICT	1489	1489	A -> S (IN REF. 2).
SO	SEQUENCE	1816	AA: 201818	MW: B49C45F3A45999D8 CRC64:

Query Match
 Best Local Similarity

5.6%; Score 168; DB 1; Length 1816;
 19.6%; Pred. No. 0.014;

Query	Subject	Score	DB	Length	Query	Subject	Score	DB	Length
QY	25 RGAGSVLPPEGGQKKEKVKTEVEDYKCEKCRVLVCPKRO--TEGGRPFESCAALLSS	82			QY	133 LVHLKNEGQFELPCLRADCKEVLKRDLRPHVCKACKYEPATCSHCKSQVPMKIKQKHE	192		
Db	358 REAENRLLLEASSIKEERRTLLDYVTRRSIVYINRVLSECRSK-----DLGGS	410			Db	411 EKPESVLERLDAVINDLESKARALDOASALEAEARRLVQALSMLESGSARCPYVG--	468		
QY	83 SSPKCTACQ--ESITIKDYKFKDNCCKRETLAQVYCR-----NEGRCAGQLTLGHL	132			QY	469 -----AELPPGRAEALAHRYRHE--AERLKKAKKEKAALAEKAKRAEASRLQDDKRRR	517		
Db	411 EKPESVLERLDAVINDLESKARALDOASALEAEARRLVQALSMLESGSARCPYVG--	468			Db	193 DTDCPCVVVSCPHKCSVQTLTR--SEL.SAHLSEC.VNAPSTCSFKRYGCVPGTNOQTIAH	250		
QY	133 LVHLKNEGQFELPCLRADCKEVLKRDLRPHVCKACKYEPATCSHCKSQVPMKIKQKHE	192			QY	518 -----IELLSRLNQLEGLRE-----LGFQTEPDLAKAE	547		
Db	411 EKPESVLERLDAVINDLESKARALDOASALEAEARRLVQALSMLESGSARCPYVG--	468			QY	251 EASSAAV--QHVLKLEKMSNLSLEKYSLLQNSYV-----EKNKSSTOSLNQOTSFELEIPIRQK	305		
QY	548 QKRLMLRRLREELKRLKENSLEEKRYNLSREVALREAKTRALEVLR--LGIKEEAR	603			Db	548 QKRLMLRRLREELKRLKENSLEEKRYNLSREVALREAKTRALEVLR--LGIKEEAR	603		
QY	306 EMLRNNSKILHLQRVINDSOAEKL-----KEL--DKE	335			QY	604 EKKTLSSESKILRMLVSKAEADLATRLGTTARSLDDLEKAREALEGVDKELSAIERR	663		
Db	604 EKKTLSSESKILRMLVSKAEADLATRLGTTARSLDDLEKAREALEGVDKELSAIERR	663			QY	336 IRPPRWMEERLSDSSVESTLQNRVTELESVDKSAGOAANNGLLESQLSRHQDTLSVHD	395		
QY	664 LEEARRLKEEAPAKLWAEQVMKRLLELEAEKELKREVSRSKSEIARLKEVONTLAEILD	723			Db	664 LEEARRLKEEAPAKLWAEQVMKRLLELEAEKELKREVSRSKSEIARLKEVONTLAEILD	723		
QY	396 IRLADMRLRFQVLETAASYNGVILMKITDYKARQEAQVMGCTLSLY	440			QY	724 DRISRIDREMGELQT-----RIKEMKSRK--ASGEALALY	757		
Db	724 DRISRIDREMGELQT-----RIKEMKSRK--ASGEALALY	757							

RC TISSUE=uterus, Ovary, and Placenta;
 RA MEDLINE=96025835; PubMed=7592654;
 RX Orimo A., Inoue S., Ikeda K., Noji S., Muramatsu M.:
 "Molecular cloning, structure, and expression of mouse estrogen-
 responsive finger protein Efp. Co-localization with estrogen receptor
 mRNA in target organs.";
 RT J. Biol. Chem. 270:24406-24413(1995).
 CC -1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: D63902; BAA09941.1; -
 DR MGI: 102749; Trlm25.
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR InterPro: IPR003878; SPRY_domain.
 DR InterPro: IPR003877; SPRY_receptor.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00622; SPRY; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00449; SPRY; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR KZING_finger; Coiled coil.
 FT 2N_FING 13 54 RING-TYPE.
 FT DOMAIN 215 305 COILED COIL (POTENTIAL).
 FT 514 631 SPRY.
 SQ SEQUENCE 634 AA; 71772 MW; 6659C9DE283E611 CRC64;
 Query Match 5.4%; Score 161; DB 1; Length 634;
 Best Local Similarity 18.5%; Pred. No. 0.011;
 Matches 75; Conservative 65; Mismatches 130; Indels 136; Gaps 17;
 QY 48 DKYKCKGRLVLCNPKOTCGHRCFSCMAALLSSSP--KCTACQESIIKDKYFKDNC 105
 DB 9 EELSCVCLLEFKPEYTPFCGHNFCSCLEDEWVGPPYRCQGR-----KVYQ--V 59
 QY 106 KREILALQVYC-----RNEGRCGEQLTLGHLVHLK-NECQ 141
 DB 60 RPOLQKWTVMCAVVEOFLAQEARPPVDMTPPARFSASSATOVACDCLTEIAVKTG- 118
 QY 142 FEELPCIRADCKEKV-----LRKDLRDHVEKAC---KYREATCSHCKSQVP 184
 DB 119 --LVCMASFQGLRLRHPEDSPAFQHPLOSPRDLIRKCKCQHNRLRREFFCP----- 168
 QY 185 MIKLQKHEDYDCPVVVSCHK-CSTVOTLLRSELNAHLECVNABSTCSFKRYGCVFOGT 243
 DB 169 -----EHQECICHICLVHEKTKCSPTTL--SQASADL----- 197
 QY 244 NQOIKAEHSSANVOHVULKEHNSLEKYSVLQNSVEKNSIOSLHNOISCFEIEIR 303
 DB 198 -----EYKLRNKLTLTHSHINGATKALEVRSKQOCQVDSMKR 235
 QY 304 OKEMLRNNSKILHLOVID-----SQAKLEKLEKDEI-----RPFQNMEEADSMKS 351
 DB 236 KMEQIR---QEYMKKAVIDAETSRLRKEBEKRYVGFDTIYQVLVKKKSEMQTKLA 292
 QY 352 SVESLQNVTELESVDKSA---GOAARNLTLLSLSQSRHDQTSVH 394
 DB 293 EVELIMDKGDEFLEKRAKLOGESTKPYIPIKIDLD-HDLIMGIV 337

AC P29616;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Myosin heavy chain, cardiac muscle isoform (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 65-1102 FROM N.A.
 RC STRAIN-Broiler; Tissue=Heart;
 RX MEDLINE=92130260; PubMed=1774788;
 RA Stewart A.F.R., Camoretti-Mercado B., Perlman D., Gupta M.,
 RA Jakovic S., Zak R.;
 RT "Structural and phylogenetic analysis of the chicken ventricular
 RT myosin heavy chain rod.";
 RL J. Mol. Evol. 33:357-366(1991).
 RN [2]
 RP SEQUENCE OF 1-259.
 RC TISSUE=Heart;
 RX MEDLINE=93039740; PubMed=1418675;
 RA Watanabe B.;
 RT "Amino-acid sequence of the short subfragment-2 in adult chicken
 RT cardiac muscle myosin.";
 RL Biol. Chem. Hoppe-Seyler 373:1045-1054(1992).
 CC -1- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC SUBUNIT: MUSCLE MYOSIN (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (RLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC -1- TISSUE SPECIFICITY: VENTRICULAR MUSCLE AND TRACED LEVELS IN THE
 CC ATRIUM. ALSO TRANSIENT EXPRESSION IN SKELETAL MUSCLE DURING FETAL
 CC DEVELOPMENT AND REGENERATION FOLLOWING FREEZE INJURY.
 CC -1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
 CC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
 CC CONSERVED.
 CC -----
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 CC -----
 DR EMBL: X59552; CAA42130.1; -
 DR HSSP: P03437; IHM.
 DR InterPro: IPR002928; Myosin_tail.
 DR Pfam: PF01576; Myosin_tail; 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW ATP-binding; Multigene family.
 FT NON_TER 1
 FT DOMAIN <1 1102 COILED COIL (POTENTIAL).
 FT CONFLICT 65 65 A -> T (IN REF. 1).
 FT CONFLICT 92 92 V -> A (IN REF. 1).
 FT CONFLICT 113 114 CS -> FAL (IN REF. 1).
 FT CONFLICT 135 135 H -> Q (IN REF. 1).
 FT CONFLICT 185 185 T -> R (IN REF. 1).
 SQ SEQUENCE 1102 AA; 128008 MW; 229368D049825DC CRC64;
 Query Match 5.3%; Score 157.5; DB 1; Length 1102;
 Best Local Similarity 20.1%; Pred. No. 0.034;
 Matches 102; Conservative 85; Mismatches 184; Indels 137; Gaps 21;

```

OY 14 QPNPPLKLDPRGAGSYLVEPGGKYKFKVYEDKCKEGRVLCNPKQTECGRCE 73
DB 591 QEDMIDLEKNSAASLKKRGF-DKILNPKKQKYESQAL-----EASOKER 641
OY 74 SCMAALSSSPKTAQOSEIITDKYFKNCKCKRELALQVCRNDEGCACQILGHL 133
DB 642 SLSTFLFKLN---AYEEL-DHL---ETLKRKNLQ---BEISDLNMQISEGKN 688
OY 134 VH-----LNKCOFE-----ELPCLRADCKEYLRKD-- 160
DB 689 LHEIEKVKQVEQKSEVQALAEAGALEHESKTIHQLELSQAKDFEKLAKDEE 748
OY 161 ---LRQHEKACKYKATC-SHCKSVPMIKLQKHEDDPCVVVSCPH----- 205
DB 749 MONIRNQQTIDSLQSTLDSKRSNEMALRLKMEGDLNMEIQLSHANRHAATKS 808
OY 206 KCSQVTLKSELS-----AHLSKCNAPSTCSFKRYGCVQGTMOQKA----- 249
DB 809 ARGLQVQIK-ELQVQVLDLGHLEDEKQVAVSDRRNN-LQSELEDELRLDQTERAK 866
OY 250 ---HEASSAVQHVNLKESNS-----LEKRVSLQNSVEYKKNKSIOSLHNOICSPFI 299
DB 867 LAEHELLEATERVNLHTQNTSLINQKKLEGDISQONEVEESIQECRNNEQAKAKAIT 926
OY 300 EIEROKEMLRNNEKTLHQRYIDQAKELKEIPEPQNNEADSM-----KSSVE 354
DB 927 DAAMAAEELKKQDTSAHLEKRNKEQITDLOKRL-----DEAQIALKGKQIOQ 979
OY 355 SLQNRVTELES-----VDRSQAQAARNTGLSELSRHDQTSVADIRPLAMDL 403
DB 980 KLESRYBELLENELNRNSDAQKARKFERIKELTYGSEDKKILA---RMDULID 1035
OY 404 RQVLETASYNGVLIWKIRDKYRKQEA 431
DB 1036 KLOL-----KVKSYKHQAEFA 1051

RESULT 12
MEPB_MOUSE
ID MEPB_MOUSE STANDARD; PRT; 704 AA.
AC 061847;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2).
GN MEPIB OR MEP-1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94012651; Pubmed=8407940;
RA Gorbea C.M., Marchand P., Jiang W., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Bond J.S.;
RT "Cloning, expression, and chromosomal localization of the mouse
RT meprin beta subunit".
RL J Biol. Chem. 268:21035-21043(1993).
RM [2]
RN SEQUENCE FROM N.A. (ISOFORM BETA').
RC TISSUE=Kidney;
RX MEDLINE=96147211; Pubmed=8567689;
RA Dietrich J.M., Bond J.S., Jiang W.;
RT "A novel meprin beta' mRNA in mouse embryonal and human colon
RT carcinoma cells.".
RL J. Biol. Chem. 271:2271-2278(1996).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of protein and peptide substrates
CC preferentially on carboxyl side of hydrophobic residues.
CC -1- COFACTOR: BINDS 1 ZINC ION.
CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH
CC IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED
CC HETERODIMERS.

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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, THE BETA AND BETA' SUBUNITS,
CC DIFFER IN THEIR N-TERMINUS DUE TO DIFFERENTIAL PROMOTER USAGE AND
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: THE BETA-SUBUNIT IS EXPRESSED IN KIDNEY,
CC INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM
CC HAS BEEN FOUND IN CARCINOMA CELLS.
CC -1- INDUCTION: By retinoic acid.
CC -1- PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS
CC ARE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: L15193; AAA75234.1; -.
DR HSSP: P28825; 1IAF.
DR MEROPS: M12.004; -.
DR MGD: MG1:96964; Meprb.
DR InterPro: IPR001506; Astacin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000998; EGF-like.
DR InterPro: IPR002083; MAM_domain.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR000130; Zn_MTpeptidse.
DR pfam: PF000629; MAM; 1.
DR pfam: PF00629; MAM; 1.
DR pfam: PF00917; MATH; 1.
DR pfam: PF01400; Astacin; 1.
DR PRINTS: PR00480; ASTACIN.
DR PRINTS: PR00020; MAMDOMAIN.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00137; MAM; 1.
DR SMART: SM00651; MATH; 1.
DR SMART: SM00235; ZnMC; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS00060; MAM_2; 1.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01166; EGF_2; FALSE_NEG.
DR Transmembrane: Hydrolase; Metalloprotease; zinc; glycoprotein;
DR Zymogen; Signal; EGF-like domain; Alternative splicing.
KW SIGNAL
FT 1
FT PROPEP 21
FT CHAIN 65
FT DOMAIN 21
FT TRANSMEM 655
FT DOMAIN 679
FT DOMAIN 693
FT DOMAIN 261
FT DOMAIN 607
FT METAL 153
FT ACT SITE 154
FT METAL 157
FT METAL 157
FT METAL 163
FT DISULFID 611
FT DISULFID 616
FT DISULFID 633
FT CARBOHYD 193
FT CARBOHYD 219
FT CARBOHYD 235
FT CARBOHYD 316
FT CARBOHYD 422
FT CARBOHYD 437
FT CARBOHYD 529
FT CARBOHYD 548
FT 548

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FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 27 MDARHQPWFVAFPLASGLAPAEKF -> MNSYAGPASR
FT SRHSFKCRMKLKLAPRDMQMYMTFG (IN ISOBOM
FT BETA').
SQ SEQUENCE 704 AA: 79548 MW: 2D010DDJ4650F70 CRC64:

Query Match
Best Local Similarity 25.1%; Score 151.5; DB 1; Length 704;
Matches 54; Conservative 38; Mismatches 56; Indels 67; Gaps 11;

DY 391 LSHVDRDLMDLRFVLETASNGVLTKIRDKRKROEAVMGKTLISQPFYTGFG 450
DY 416 LSTDDINLSETRCPNH-----IWHQNF-----TQLIGGQDTYSSEPTSSK-G 459
DY 451 YKCAVYVINGDMGKGTSLFVYIMRGEYDALLPMPFK-QKVTLMLNDQ----- 500
DY 460 YAF-QIYND---LRYSTVNGVIFHLISGANDQLOMPQQAQATLTDQNPDIRQRMF 514
DY 501 -----GS-----SRHLDARFDPNSSFKKFPGEMNIASGCPYFVQ 539
DY 515 NQSIITDPTMTSDNGSYFMDRPSKVGVDVF---PNCQFSR-----GIGYGVTVFTR 566
DY 540 TVLENGTVIKDRIFIKVIYD-----TSDDLDP 567
DY 567 ERLKREFIKGDDIYILLVYEDISLNSSTAVDP 601

RESULT 13
YD86 SCHPO STANDARD; PRT: 1957 AA.
AC Q10411:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein Clf3.06c in chromosome I.
OS SPAC1F3.06c.
ON Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRAIN-972:
RX MEDLINE-21848401; PubMed-11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolckele E., Aert R., Robben J., Gymnopoulos B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreesen S., Gloux S., Leleux V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Sipkavski G.V., Ussery D., Barrett B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
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CC
CC EMBL; 270690; CAA94624.1; -.
CC Hypothetical protein.
KW SEQUENCE 1957 AA: 222785 MW: 3F480CA06171D9DA CRC64:

Query Match
Best Local Similarity 20.4%; Score 149; DB 1; Length 1957;
Matches 105; Conservative 77; Mismatches 166; Indels 166; Gaps 22;

DY 39 KEKVEYVEDKYKCEKRCVLNCPKQTECGHFCSCMAALLSSSPKTAQCEST----- 94
DY 1416 KESLISLEES-----LSNOROKESSLLDAKNELEHMLDTSRKNSSLMKEISIN 1466
DY 95 --IKDKVKNCKCKREILALQVYCNREGCAEQDILGHLVHLKNCQFELPCLRAD- 151
DY 1467 SLDKSEFLASAVEKLGALD-KLHSESLAMEIK--SQLEAKKEKIQVESTIOELDI 1523
DY 152 -----CKEVLKRLDLDHYEAKKYREATCSHCKSQVPIKQKHED----- 193
DY 1524 ETTAKNNYEKLNKDKSIIR-DLSENIQL-----NNLAEKSAVKRLSTKESEILQF 1578
DY 194 ---TDPCVYVSCPHKCSVOGTL-RSELSAHLSECVNASTCSFKKRCYFOGTNOQIK 248
DY 1579 NSRLADLEY-----HKQVSESLGRSLK-----LASTTEELQ 1611
DY 249 AHE-----ASSAVOHVNLKEMSN-----SLEKYSVLONESVEKKNSTOS 289
DY 1612 LAENERSLITRMELQOVADLSNKSLSLSDRLTSLSDSVASLQKECKISNTYES 1671
DY 290 LHNQICS-----FEIEROKEMLRNNEKTIHLQVIDSQAELKELDEIRPFPRON 342
DY 1672 LDVLTVOARNAELEDEVSRSVDKIRRDCEHL-----SGKLKLLSOLEQHEH 1724
DY 343 WEADSMKSSVSLNRTYTESLVKSSAQARNTGLLESQLSRDRDLSVHDLRLAMD 402
DY 1725 FFRAE-----OQRMQL-----GFLKETVYKQKELKLNLNLEQDIL 1761
DY 403 LRFQVLEFASVNGVLWIKRDYKRR--KQEAVMGKTLISVQPFYTGFGYKMCARVYL 459
DY 1762 PRSSILVYEST-----IROLKEKILYQERLNLIEL-----SQQLPKYFGV----- 1803
DY 460 NGDGMKGKGTSLFVYIMRGEYDALLPMPFKOV 493
DY 1804 -----FFKTNRVEMEVL--DSFKQOV 1822

RESULT 14
LMA4_HUMAN STANDARD; PRT: 1816 AA.
AC Q16363; Q15335; Q14735; Q9UE18; Q9UJN9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-4 chain precursor.
GN LMA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal Lung;
RX MEDLINE-95300971; PubMed-7781776;
RA Iivanainen A., Salnio K., Sariola H., Tryggvason K.;
RA "Primary structure and expression of a novel human laminin alpha 4
RA chain.";
RL FEBS Lett. 365:183-188(1995).
CC

```

RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE=97454279; PubMed=9310354;
 RA Richards A.J., Lucarini C., Pope F.M.;
 RT "The structural organisation of LAMA4, the gene encoding laminin
 alpha4.";
 RL Eur. J. Biochem. 248:15-23(1997).
 RN (3)
 RP SEQUENCE OF 236-1816 FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE=95048381; PubMed=7959779;
 RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
 RA Pope F.M.;
 RT "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
 RT a partial cDNA encoding a variant laminin A chain.";
 RL Genomics 22:237-239(1994).
 RN (4)
 RP SEQUENCE OF 66-1816 FROM N.A.
 RA Tubby B.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
 CC MEMBRANES (MAJOR COMPONENT).
 CC -1- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG,
 CC OVARY SMALL AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO
 CC EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE,
 CC BRAIN. HIGH EXPRESSION IN PERIL LUNG AND KIDNEY. EXPRESSION IN
 CC FETAL AND MEMBRAN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS
 CC IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
 CC -1- SIMILARITY: CONTAINS 3.5 LAMININ G-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
 CC -1- CAUTION: GENE LAMA4 WAS FORMERLY CALLED LAM3.
 CC
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 DR EMBL: S78569; AAB34635.1; -
 DR EMBL: X91171; CAA62596.1; -
 DR EMBL: Y14240; CAA74636.1; -
 DR EMBL: X74939; CAA54258.1; -
 DR EMBL: Z89289; CAB16553.1; -
 DR HSSP: P02468; IKIO.
 DR GeneW: HGNC:6484; LAMA4.
 DR MIM: 600133; -
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00053; Laminin_EGF; 6.
 DR Pfam: PF00054; Laminin_G; 6.
 DR SMART: SM00180; EGF_Lam; 3.
 DR SMART: SM00282; LamG; 5.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 3.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
 KW Glycoprotein; Basement membrane; Extracellular matrix; coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT	SIGNAL	1	24	POTENTIAL.
FT CHAIN		25	1816	LAMININ ALPHA-4 CHAIN.
FT DOMAIN		82	131	LAMININ EGF-LIKE 1.
FT DOMAIN		132	186	LAMININ EGF-LIKE 2.
FT DOMAIN		187	240	LAMININ EGF-LIKE 3.
FT DOMAIN		241	255	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN		256	825	DOMAIN II AND I.
FT DOMAIN		826	1028	LAMININ G-LIKE 1.
FT DOMAIN		1040	1220	LAMININ G-LIKE 2.
FT DOMAIN		1227	1395	LAMININ G-LIKE 3.
FT DOMAIN		1462	1633	LAMININ G-LIKE 4.
FT DOMAIN		1640	1813	LAMININ G-LIKE 5.
FT DOMAIN		313	396	COILED COIL (POTENTIAL).
FT DOMAIN		466	521	COILED COIL (POTENTIAL).
FT DOMAIN		574	607	COILED COIL (POTENTIAL).
FT DOMAIN		655	717	COILED COIL (POTENTIAL).
FT DOMAIN		770	799	CELL ATTACHMENT SITE (POTENTIAL).
FT SITE		717	719	BY SIMILARITY.
FT DISULFID		82	91	BY SIMILARITY.
FT DISULFID		84	98	BY SIMILARITY.
FT DISULFID		101	110	BY SIMILARITY.
FT DISULFID		113	129	BY SIMILARITY.
FT DISULFID		132	146	BY SIMILARITY.
FT DISULFID		134	155	BY SIMILARITY.
FT DISULFID		157	166	BY SIMILARITY.
FT DISULFID		169	184	BY SIMILARITY.
FT DISULFID		187	202	BY SIMILARITY.
FT DISULFID		189	209	BY SIMILARITY.
FT DISULFID		212	221	BY SIMILARITY.
FT DISULFID		224	238	BY SIMILARITY.
FT DISULFID		266	266	INTERCHAIN (PROBABLE).
FT DISULFID		269	269	INTERCHAIN (PROBABLE).
FT CARBOHYD		104	104	N-LINKED (GLCNAC. . .)
FT CARBOHYD		215	215	N-LINKED (GLCNAC. . .)
FT CARBOHYD		308	308	N-LINKED (GLCNAC. . .)
FT CARBOHYD		458	458	N-LINKED (GLCNAC. . .)
FT CARBOHYD		524	524	N-LINKED (GLCNAC. . .)
FT CARBOHYD		550	550	N-LINKED (GLCNAC. . .)
FT CARBOHYD		571	571	N-LINKED (GLCNAC. . .)
FT CARBOHYD		574	574	N-LINKED (GLCNAC. . .)
FT CARBOHYD		631	631	N-LINKED (GLCNAC. . .)
FT CARBOHYD		639	639	N-LINKED (GLCNAC. . .)
FT CARBOHYD		735	735	N-LINKED (GLCNAC. . .)
FT CARBOHYD		751	751	N-LINKED (GLCNAC. . .)
FT CARBOHYD		754	754	N-LINKED (GLCNAC. . .)
FT CARBOHYD		780	780	N-LINKED (GLCNAC. . .)
FT CARBOHYD		803	803	N-LINKED (GLCNAC. . .)
FT CARBOHYD		1086	1086	N-LINKED (GLCNAC. . .)
FT CARBOHYD		1281	1281	N-LINKED (GLCNAC. . .)
FT CARBOHYD		1359	1359	N-LINKED (GLCNAC. . .)
FT CARBOHYD		1411	1411	N-LINKED (GLCNAC. . .)
FT CONFLICT		143	143	N-LINKED (GLCNAC. . .)
FT CONFLICT		178	178	A -> P (IN REF. 1).
FT CONFLICT		265	265	L -> F (IN REF. 1).
FT CONFLICT		276	276	G -> GMDPPTS (IN REF. 4).
FT CONFLICT		491	491	D -> A (IN REF. 4).
FT CONFLICT		1057	1057	Y -> H (IN REF. 2 AND 3).
FT CONFLICT		1110	1112	T -> P (IN REF. 1).
FT CONFLICT		1110	1112	SGR -> GGP (IN REF. 4).
SEQ		1816 AA;	201908 MW;	04E9AR379A0FAAD CAC64;

Query Match 4.98; Score 147; DB 1; Length 1816;
 Best Local Similarity 19.38; Pred. No. 0.26;
 Matches 100; Conservative 81; Mismatches 206; Indels 132; Gaps 25;

Oy 16 NPLKLPDRGAGSVIVPEGGYKKEKRYVCKEKRVLVCNPKQDEG--GHFCE 73
 Db 46 DPPTSETP-RVALGRPLPAAEKCNAGFFHTLSG--ECVPCD--CNGNSNECLDGSQYCV 99
 Oy 74 SCMAALLSSSPKCTACQESIIKDKV-----FKDNC-----CKREIALOVY 115
 Db 100 HCGR---NTTGEHCEKCLDGTIGDSINGAQFOCPGCCPLPLHANFAESCTRRKNGAVRCI 156
 Oy 116 CRNCGRG-----CAEQTLTGLHLVHLKNECOFEEELPLRADCK---EKVLRRDLRDHYE 166

Db 603 KEITVWVEKHKTELES-----KHQDALTWTEKIQYVKQOY 638

OY 445 YT 446

Db 639 QT 640

Search completed: December 19, 2002, 15:00:48
Job time : 19 secs